Quantitative microbial risk assessment of adenovirus and *Ascaris* in FOGO and GO composts

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1. Project scope and objective

In December 2020 and January 2021, the NSW Environment Protection Authority (EPA) conducted a sampling campaign ('FOGO_GO'). This campaign covered 21 facilities producing food organic and garden organic (FOGO) compost, garden organic (GO) compost or dehydrated food waste. The EPA had discrete ('grab') samples taken from these facilities analysed for a wide range of contaminants, including selected microbial pathogens representing bacteria, viruses and helminths (intestinal worms). The FOGO_GO sampling campaign complemented a previous sampling campaign ('FOMO for FOGO') carried out over May and June 2019 covering 10 facilities producing FOGO compost. Samples from the FOGO_GO campaign and the FOMO for FOGO campaign were analysed for a common suite of microbial pathogens. Analytical data from the 2 campaigns were summarised by the EPA and provided to the Environment, Energy and Science Group[1] – Contaminants and Risk Team (C&R) of the Department of Planning and Environment for assessment.

C&R assessed the analytical data provided and developed quantitative microbial risk assessment (QMRA) modelling for selected microbial pathogens identified as being of primary concern for human health.

1.1 Limitations

C&R has used the data provided by the EPA for risk assessment. It is assumed that the data provided are an accurate summary of the analytical results received by the EPA, and that appropriate quality assurance/control of the analytical results has been performed by the laboratories that tested the samples.

2. Key findings and recommendations

The QMRA modelling developed by C&R was peer-reviewed by an acknowledged international QMRA expert. In the reviewer's opinion, 'the QMRA models have been constructed according to best practise and represent a systematic and clear implementation of the QMRA framework for assessing the safety of the FOGO compost products'.

C&R's review of the analytical data provided by the EPA identified adenovirus and *Ascaris* ova as the 2 microbial pathogens that justified further assessment using QMRA. These pathogens were present in sufficient numbers in FOGO and GO compost, and both are also used as 'reference pathogens' representing viruses and helminths respectively. Sufficient information about dose–response, illness outcomes and disease burden is available in the scientific literature to support detailed QMRA of these 2 pathogens.

The helminth *Taenia* was also frequently detected in FOGO and GO compost. Similarly, microbial pathogen data from the FOGO_GO campaign showed Taenia was also routinely detected in the dehydrated food waste, and *B. cereus* spores were also detected occasionally. Currently the scientific literature for either *Taenia* or *B. cereus* is not sufficiently developed to provide the information needed for QMRA. C&R notes the ongoing work needed to be able to assess these pathogens and did not assess either by QMRA.

[1] now known as the Environment and Heritage Group

QMRA was carried out by C&R for adenovirus and *Ascaris* ova, based on data provided for FOGO and GO compost, and using 5 exposure scenarios representing typical end uses of the compost.

Adenovirus:

- Viral pathogens present the highest risk to human health in FOGO and GO composts based on the microbiological sampling results and subsequent QMRA. The levels of adenovirus consistently resulted in a high likelihood (up to 99%) of exceeding the health-based target for all 5 exposure scenarios modelled, indicating a probable risk of harm to human health.
- Adenoviruses are pathogens of human origin so would not be expected to routinely be in the source material accepted by facilities to make either FOGO or GO compost. The potential sources of this pathogen need to be investigated and strongly suggest human faecal (e.g. wastewater or sludge) contamination.

Ascaris:

- The quantified health risk associated with *Ascaris* was lower than that for adenovirus. The levels of *Ascaris* ova were shown by QMRA to be unlikely to exceed the health-based target in 2 of the 5 scenarios modelled. There was a marginal–low likelihood (0.1–14%) of exceeding the health-based target in the other 3 exposure scenarios, indicating a possible risk of harm to human health.
- Human infection with *Ascaris* is by ingestion of ova via the faecal–oral route. It is possible that ova could be associated with food used to produce FOGO compost, but non-food sources would also have to be investigated to explain the presence of *Ascaris* ova in GO compost. Material of faecal origin would not be expected to routinely be in the source material accepted by facilities to make either FOGO or GO compost. These findings are a further indication of human faecal (e.g. sludge or faeces) contamination.

Overall C&R concludes that there is a potential risk of harm to human health from microbial pathogens in the FOGO and GO compost, primarily due to the levels of adenovirus, with a relatively minor contribution from *Ascaris* ova. The presence of both of these faecal-related pathogens in the compost produced highlights the need for further characterisation of the source material, including potential faecal contamination.

2.1 Recommendations

C&R recommends further assessment and characterisation of:

- **the sources of the FOGO and GO feedstock** – a desk-based review of facility records combined with scientific literature is needed to identify the sources of microbial pathogens of concern coming into the facilities
- **composting processes prior to the final compost product** – in particular, there is scope for operational composting conditions to be better monitored by the facilities and reported to the EPA, to verify sufficient time–temperature profiles have been achieved to routinely inactivate microbial pathogens of concern to levels that do not pose an unacceptable risk to human health.

3. Assessment of analytical data for microbial pathogens in FOGO and GO compost

Data from both sampling campaigns for FOGO and GO compost included sampling and analysis of a range of microbial pathogens representing bacteria, viruses and helminths (intestinal worms). Analytical data for microbial pathogens in FOGO (2019 and 2020–21) and GO (2020–21) composts are summarised in Appendix A.

3.1 Bacteria

A range of bacteria relevant to human health were targeted for analysis, covering human pathogens (*Salmonella* and *Legionella* spp.) and spore forming bacteria (*Bacillus cereus* and *Clostridium perfringens*). A reference organism (*Campylobacter*) was also included that could be used as a representative pathogen if detected, as sufficient information about dose–response, illness outcomes and disease burden is available in the scientific literature to support detailed QMRA. Bacterial indicator organisms (thermotolerant coliforms and *E. coli*) were also measured, as the presence of these organisms is indicative of human pathogens and they are nominated (with maximum limits) in the Compost Resource Recovery Order (RRO) (EPA 2016).

The human pathogens *Salmonella* and *Legionella* spp. were absent, as was the reference pathogen *Campylobacter*. Spores of *B. cereus* and *C. perfringens* were occasionally detected. The relevance of these spore forming organisms is subject to a separate ongoing assessment by C&R and the EPA, considering potential risk to human health, but also as indicators of the operating conditions of the composting processes. Consequently, C&R did not assess any individual bacterial pathogens further using QMRA.

There were occasional detections of thermotolerant coliforms and *E. coli* in the FOGO and GO compost from the 2020–21 samples, though all were within the levels that complied with the requirements outlined in the Compost RRO. The levels of thermotolerant coliforms in FOGO compost from the 2019 samples exceeded the 1,000 MPN/g (most probably number per gram) required in the Compost RRO in 5 of the samples, representing 3 of the facilities tested. While these levels are potentially of concern as an indicator of faecal contamination of the compost, the levels of *E. coli* are significantly lower and within the level of 100 MPN/g required in the Compost RRO. *E. coli* is the most common thermotolerant coliform present in faeces, and can be considered as the more suitable and reliable indicator of faecal contamination.

Comparing the bacterial indicator organisms between sampling campaigns, the thermotolerant coliforms are significantly (1–2 orders of magnitude) higher in the 2019 (FOGO) samples compared to the 2020–21 samples (FOGO and GO), whilst the *E. coli* levels are relatively comparable. This inconsistency between results for thermotolerant coliforms might be a consequence of the different methodologies used. The Compost RRO has requirements for a method for ‘faecal coliforms’ (AS 5013.3, Standards Australia 2009); however, this method is for the detection and enumeration of total coliforms, not thermotolerant (or ‘faecal’) coliforms. Communication with the third-party analytical provider identified that the data reported as thermotolerant coliforms were derived from a test method for the detection and enumeration of *E. coli* (AS 5013.15, Standards Australia 2006), modified in-house to include enumeration of thermotolerant coliforms. This is technically defensible as an interim measure, but the ambiguity over nominated methods, combined with the reliance on an in-house modification of a published method, introduces some uncertainty, possibly limiting interpretation of the results for thermotolerant coliforms. It is recommended that a published method that

explicitly enumerates thermotolerant coliforms in compost (or a comparable solid material) is identified and promulgated in a future revision of the Compost RRO.

3.2 Viruses

A selection of virus groups (adenovirus, enterovirus and reovirus) were nominated for analysis, representing a range of virus families that are relevant to human health. In addition, adenoviruses are sufficiently persistent and infectious to humans that they can also be used as a reference pathogen for viruses, representing a conservative assessment of all viruses relevant to human health.

Adenoviruses are viruses that belong to the family *Adenoviridae*, and collectively are referred to as adenovirus. They cause a wide variety of illnesses in humans including eye infections, respiratory infections and diarrhea. There are currently 57 known types of adenovirus known to cause human infection, with most human illness associated with approximately one third of the adenovirus types (Haas et al. 2014). Adenovirus is also used as a reference pathogen representing enteric viruses, as sufficient information about dose–response, illness outcomes and disease burden is available in the scientific literature to support detailed QMRA.

Adenovirus was the virus group mainly detected, with the occasional detection of enterovirus. Reovirus was not detected. In this case, assessment of the potential risk of harm to human health due to adenovirus would also represent enterovirus. Consequently, C&R assessed adenovirus using QMRA.

3.3 Helminths

The 2 most common helminths of the genera *Taenia* and *Ascaris* were nominated for analysis, via counting of ova (eggs) in the compost. *Ascaris* is also used as a reference pathogen representing helminths, as these ova are persistent in the environment and sufficient information about dose–response, illness outcomes and disease burden for *A. lumbricoides* is available in the scientific literature to support detailed QMRA.

Helminths are parasitic worms, and are among the most common causes of chronic infections in humans globally. Helminths have a complex lifecycle often involving other animals. For example, helminths of the genus *Taenia* infect cattle (*T. saginata*) and pigs (*T. solium*). These pathogens can be transmitted to humans by ingestion of raw or inadequately cooked animal flesh containing ova. The ova then develop into tapeworms inside the human host, resulting in the formation of more ova that are passed out in the faeces of humans infected with the adult worm, completing the cycle back into the environment (Hird and Pullen 1979).

Helminths of the genus *Ascaris* also cause disease in animals, infecting humans (*A. lumbricoides*) and pigs (*A. suum*). Hosts contract *Ascaris* infection via the faecal–oral route. The human pathogen *A. lumbricoides* is transmitted by the ingestion of ova. Once ingested, each larva is released into the intestine and travels to various parts of the human body (bloodstream, lungs, trachea and pharynx) resulting in adult worms (male and female) developing inside the small intestine. The adult worms mate and the ova produced are excreted in the faeces. Once in the environment *Ascaris* ova are resistant to desiccation and can survive for up to 15 years under favourable conditions. The ova are also very sticky and can attach to fruit, vegetables and soil particles (Scott 2008).

Ova of *Taenia* were routinely detected in both sampling campaigns in 2019 and 2020–21. Ova of *Ascaris* were also detected but less frequently than *Taenia*. Assessment of both *Taenia* and *Ascaris* would have been preferable, but the scientific literature for *Taenia* is not sufficiently developed to provide the information needed for QMRA. Consequently, C&R assessed *Ascaris* using QMRA; however, if more information about dose–response, illness outcomes and disease burden for *Taenia* becomes available in the scientific literature, QMRA of *Taenia* would also be justified in a future assessment.

4. Microbial pathogen analytical data in dehydrated food waste compost

Microbial pathogen data from the FOGO_GO campaign showed ova of the helminth *Taenia* were routinely detected in the dehydrated food waste compost (data not included in this report). *B. cereus* spores were also occasionally detected.

C&R notes the ongoing work needed to be able to assess these pathogens and did not assess either by QMRA, consistent with the reasoning presented for FOGO and GO compost.

5. Quantitative microbial risk assessment

The overall aim of QMRA is to enable consideration of the measured levels of pathogens in the compost samples in the context of potential risk to human health. Further details on the QMRA are provided below. Five exposure scenarios were developed to represent a range of common domestic and commercial agricultural uses of compost (Table 1):

- 3 scenarios representing residential use, for use in the home garden for planting, growing food and potting plants
- 2 scenarios representing commercial-scale agricultural use.

Table 1 Exposure scenarios modelled for human health risk assessment

Exposure scenarios: end uses of compost				Human receptor	Exposure pathway
1	Home garden	Surface incorporated[a] (hand tilling)	Plants	Resident	Hands => ingestion
2	Home garden	Surface incorporated[a] (hand tilling)	Home garden crops	Resident	Hands => ingestion PLUS unwashed vegetables => ingestion
3	Home garden	Pots (compost only)	Plants	Resident	Hands => ingestion
4	Agricultural	Field incorporated[b] (10 cm depth)	Crops	Farmworkers[c]	Hands => ingestion
5	Agricultural	Field incorporated[b] (10 cm depth)	Crops	Public consumers	Unwashed vegetables => ingestion

[a] 'Surface incorporated' represents home garden tilling by hand using garden tools such as hand trowels.

[b] 'Field incorporated' represents commercial agricultural practices of incorporation using farm machinery.

[c] For commercial agriculture it is reasonable to assume only adults as farmworkers would be exposed.

QMRA was carried out for adenovirus and *Ascaris* ova, using these 5 exposure scenarios. The results from sampling and analysis from the 2 sampling campaigns created a representative dataset for each of these 2 pathogens (sample locations were de-identified). All 'non detect' readings were converted to zero values for the purpose of fitting statistical distributions to the data for modelling. This is important, as exposure to zero levels of the pathogens is a realistic event and needs to be included in the QMRA modelling.

5.1 Key principles of QMRA: probability of infection and illness

Potential risk of infection and illness was determined for each of the 5 exposure scenarios. This considers the probability of human infection (residents, farmworkers or the general public) once exposed to microbial pathogens in the compost. Data derived from epidemiology are used to determine the dose–response relationship for each microbial pathogen. Importantly, there is a probability of infection at any dose, as each single organism has the potential to initiate infection. The 'single hit' theory is adopted within current QMRA methodology, replacing an historical assumption that an 'infectious dose' is required for infection to occur (Hass et al. 2014).

The probability of infection is then combined with the probability of becoming ill as a result of infection. For each pathogen, there are a range of illness outcomes varying in severity and duration. These illness outcomes are characterised within QMRA, to compare to a health-based target. The Disability Adjusted Life Year (DALY) is used as the health-based metric to weight illness outcomes in QMRA.

5.2 Disability Adjusted Life Year

The DALY is a measure of population health that incorporates the different severities and durations associated with various illnesses for that fraction of the population made ill due to infection. The DALY has been applied as a metric internationally within the World Health Organization (WHO) guidelines *Quantitative microbial risk assessment: Application for water safety management* to provide a different relative weighting to pathogens based on severity of disease outcomes (WHO 2016). This approach has also been adopted in Australia within the National Water Quality Management Strategy (NWQMS) in the *Australian guidelines for water recycling: Managing health and environmental risks (Phase 1)* (NRMMC-EPHC-AHMC 2006).

One DALY represents the loss of one healthy life year. The DALY is an indicator of the time lived with a disability and the time lost due to premature death:

$$DALY = YLD+YLL$$

where

YLD = years of life lived with a disability (illness or injury)

YLL= years of life lost due to premature death.

A disease burden of 1 DALY per 10^6 people per year is an established health-based target (NRMMC-EPHC-AHMC 2006; WHO 2016). In QMRA this represents the incremental loss of one healthy life year resulting from a million people exposed to a microbial pathogen. Mathematically this translates to $1x10^{-6}$ DALY per person per year (one micro-DALY or 1 µDALY) and is adopted in this QMRA as an appropriate health-based target. A disease burden greater than 1 µDALY indicates a potential unacceptable risk to human health, requiring further consideration and investigation.

5.3 International context and peer-review of the QMRA methodology

The QMRA methodology used in this assessment was developed by C&R for assessment of microbial pathogens in compost. This is novel science and is based on internationally accepted QMRA methodology developed as an assessment framework for the water industry (WHO 2016).

The initial QMRA methodology developed by C&R for adenovirus and *Ascaris* from the 'FOMO for FOGO' 2019 campaign was peer-reviewed by an acknowledged international QMRA expert. Revision of the methodology incorporated all of the reviewer comments, as well as modifying some assumptions in the original QMRA models to align with agreed assumptions used in the C&R chemical risk assessment of PFAS and PBDEs levels in FOGO and GO compost from the FOGO_GO sampling campaign. The revised C&R QMRA methodology was subsequently used in this assessment.

5.4 Monte Carlo analysis using @Risk modelling software with Excel

For each pathogen assessed, a distribution curve was fitted (using @Risk v8.1) that statistically represents the full datasets for FOGO (2019 and 2020–21) and GO (2020–21). This includes all the 'non-detects' as zeros, to ensure the dataset is fully representative of the range of pathogen levels measured. A number of other parameters in the QMRA models are also represented by statistical distributions, to allow for a range of possible values. The risk calculations are performed iteratively (70,000 iterations, optimised in @Risk for convergence) to simulate all possible outcomes from exposure to the FOGO/GO compost, across all 5 exposure scenarios. The output from each simulation is a range of possible DALY health-based outcomes, represented as a cumulative statistical distribution. The distribution of possible DALY outcomes is then compared to 1 µDALY, to determine the likelihood of exceeding this health-based target.

5.5 QMRA of adenovirus and *Ascaris* ova

Results from the QMRA are presented for adenovirus (Table 2) and *Ascaris* ova (Table 3). The likelihood (%) of exceeding the health-based target of 1 µDALY is shown for each exposure scenario modelled. Exposure of both adults and children is considered relevant for 4 of the 5 exposure scenarios; however, for commercial agriculture (exposure scenario 4) it is reasonable to assume only adults as farmworkers would be exposed. For ease of interpretation, the values are coloured to illustrate:

- does not exceed the health-based target (green)
- marginal–low likelihood of exceeding the health-based target (orange), indicating a possible risk of harm to human health
- high likelihood of exceeding the health-based target (red), indicating a probable risk of harm to human health. Follow-up investigation is needed to identify the potential source(s) of the pathogen(s) coming into the facilities, combined with assessment of the compost treatment processes to remove the pathogen(s) of concern.

Adenovirus

The levels of adenovirus result in a high likelihood of exceeding the 1 µDALY health-based target for most of the exposure scenarios modelled, for FOGO compost from the 2 seasons (2019 and 2020–21) and for GO compost.

Table 2 **Likelihood (%) of exposure to adenovirus exceeding the health-based 1 µDALY target**

Exposure scenario	FOGO 2019		FOGO 2020–21		GO 2020–21	
	Adult	Child	Adult	Child	Adult	Child
1	61	86	38	76	84	95
2	88	94	76	93	96	99
3	93	94	88	93	98	99
4	94	ND	87	ND	98	ND
5	12	20	1.0	3.5	48	57

ND = child exposure not determined for this scenario, as it is assumed fulltime farmworkers are adults.

Discussion with the contracted laboratory confirmed that the adenovirus levels identified in their analyses infect human cell lines representing receptor cells relevant to human infection, with further analysis by polymerase chain reaction (PCR) techniques using primers for adenovirus that infect humans. These 2 lines of evidence demonstrate viable and infective adenoviruses that are of human origin and are directly relevant to human health.

C&R concludes that adenovirus levels in FOGO and GO compost indicate a probable risk of harm to human health. This finding is surprising, as adenoviruses are human pathogens of faecal origin so would not be expected to routinely be in the source material accepted by facilities to make either FOGO or GO compost.

Ascaris ova

The levels of *Ascaris* ova are unlikely to exceed the 1 µDALY health-based target in 2 of the exposure scenarios assessed, for FOGO compost from the 2 seasons (2019 and 2020–21) and for GO compost. Use of FOGO in home gardens (Exposure scenario 2), FOGO and GO in home garden pots (Exposure scenario 3) and FOGO in agriculture (Exposure scenario 4) indicate a marginal–low likelihood of exceeding the health-based target for adults. Children are potentially at a higher risk from using FOGO compost for plant potting.

Table 3 **Likelihood (%) of exposure to Ascaris ova exceeding the health-based 1 µDALY target**

Exposure scenario	FOGO 2019		FOGO 2020–21		GO 2020–21	
	Adult	Child	Adult	Child	Adult	Child
1	0.0	0.0	0.0	0.0	0.0	0.0
2	0.0	0.8	0.0	0.0	0.0	0.0
3	4.1	14	0.4	3.4	0.1	1.6
4	4.2	ND	0.3	ND	0.0	ND
5	0.0	0.0	0.0	0.0	0.0	0.0

ND = child exposure not determined for this scenario, as it is assumed fulltime farmworkers are adults.

Discussion with the contracted laboratory confirmed that the *Ascaris* ova identified in their analyses represent viable ova that are directly relevant to human health.

C&R concludes that *Ascaris* ova are at levels in FOGO and GO compost that indicate a possible risk of harm to human health, though the risk is marginal and minor compared to that posed by adenovirus. Human infection with *Ascaris* is by ingestion of ova via the faecal–oral route. It is possible that ova could be associated with food used to produce FOGO compost, but non-food sources would also have to be investigated to explain the presence of *Ascaris* ova in GO compost. Material of faecal origin would not be expected to routinely be in the source material accepted by facilities to make either FOGO or GO compost.

5.6 Conclusion

Overall C&R concludes that there is a potential risk of harm to human health from microbial pathogens in the FOGO and GO compost, primarily due to the levels of adenovirus, with a relatively minor contribution from *Ascaris* ova. The presence of both of these faecal-related pathogens in the compost highlights the need for further characterisation of the source material, including potential faecal contamination.

6. Recommendations

The levels of adenovirus and *Ascaris* ova in FOGO and GO compost support further assessment and characterisation of:

- **the sources of the FOGO and GO feedstock** – a desk-based review of facility records combined with scientific literature is needed to identify the sources of microbial pathogens of concern coming into the facilities
- **composting processes prior to the final compost product** – in particular, there is scope for operational composting conditions to be better monitored by the facilities and reported to the EPA, to verify sufficient time–temperature profiles have been achieved to routinely inactivate microbial pathogens of concern to levels that do not pose an unacceptable risk to human health.

7. References

Standards Australia (2006) *AS 5013.15: Food microbiology Method 15: Microbiology of food and animal feeding stuffs – Horizontal method for the detection and enumeration of presumptive* Escherichia coli *– Most probable number technique*, Standards Australia, 2nd edition.

Standards Australia (2009) *AS 5013.3: Food microbiology Method 3: Microbiology of food and animal feeding stuffs – Horizontal method for the detection and enumeration of coliforms – Most probable number technique*, Standards Australia.

EPA (Environment Protection Authority) (2016) *Resource Recovery Order under Part 9, Clause 93 of the Protection of the Environment Operations (Waste) Regulation 2014: The compost order 2016*, NSW Environment Protection Authority, www.epa.nsw.gov.au/~/media/EPA/Corporate%20Site/resources/wasteregulation/RRO16-compost.ashx

Haas CN, Rose J and Gerba C (2014) *Quantitative Microbial Risk Assessment*, Wiley, 2nd edition.

Hird DW and Pullen MM (1979) 'Tapeworms, meat and man: a brief review and update of the cysticercosis caused by *Taenia saginata* and *Taenia solium*', *Journal of Food Protection*, 42(1):58–64.

NRMMC-EPHC-AHMC (2006) *Australian Guidelines for Water Recycling: Managing Health and Environmental Risks (Phase 1)*, Natural Resource Management Ministerial Council, Environment Protection and Heritage Council and the Australian Health Minister's Conference, www.waterquality.gov.au/sites/default/files/documents/water-recycling-guidelines-full-21.pdf [PDF 2.1MB]

Scott ME (2008) '*Ascaris lumbricoides*: a review of its epidemiology and relationship to other infections', *Annales Nestle*, 66:7–22.

WHO (World Health Organization) (2016) *Quantitative microbial risk assessment: Application for water safety management*, World Health Organization, www.who.int/publications/i/item/9789241565370

Appendix A: Microbiological analytical results

Table A1 Microbiological results for FOGO 2019 sampling

Sampling round	Organic waste group	De-identified facility / unit code	De-identified sample code	Sample depth	Group 17 - Bacteria and bacterial indicators										Group 18 - Helminths		Group 19 - Viruses			
					Clostridium perfringens	*Bacillus cereus*	*Salmonella* spp.	*Campylobacter* spp.	*Legionella* not *L.pneumophila*	*Legionella pneumophila* SG1	*Legionella pneumophila* SG2-15	Total *Legionella* Count	Thermotolerant Coliforms	*Escherichia coli*	*Taenia* sp. ova (intact eggs)	*Ascaris* sp. ova (intact eggs)	Enteroviruses	Adenoviruses	Reoviruses	Noroviruses
					CFU/g	CFU/g	/25g	CFU/g	CFU/mL	CFU/mL	CFU/mL	CFU/mL	MPN/g	MPN/g	/20 g (2019) /40g (2020/21)	/20 g (2019) /40g (2020/21)	/20 g (2019) /40g (2020/21)	/20 g (2019) /40g (2020/21)	/20 g (2019) /40g (2020/21)	/10g
2019	FOGO	A	FOGO-2019-A-1	30	<10	<100	ND	ND	<10	<10	<10	NT	**23**	<3	**7**	<1	<1	<1	<1	ND
2019	FOGO	A	FOGO-2019-A-2	30	<10	<100	ND	ND	<10	<10	<10	NT	<3	<3	NT	NT	NT	NT	NT	NT
2019	FOGO	A	FOGO-2019-A-3	n/a	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT
2019	FOGO	A	FOGO-2019-A-4	n/a	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT
2019	FOGO	A	FOGO-2019-A-5	60	<10	<100	ND	ND	<10	<10	<10	NT	<3	<3	<1	<1	<1	<1	<1	ND
2019	FOGO	A	FOGO-2019-A-6	60	<10	<100	ND	ND	<10	<10	<10	NT	<3	<3	NT	NT	NT	NT	NT	NT
2019	FOGO	B	FOGO-2019-B-1	30	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	**8**	**2**	<1	**35**	<1	ND
2019	FOGO	B	FOGO-2019-B-2	30	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	**4**	<1	<1	<1	<1	ND
2019	FOGO	B	FOGO-2019-B-3	60	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	**2**	<1	<1	**27**	<1	ND
2019	FOGO	B	FOGO-2019-B-4	60	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	**2**	<1	<1	<1	<1	ND
2019	FOGO	C	FOGO-2019-C-1	30	<10	**>300000**	ND	ND	<10	<10	<10	NT	**>1100**	**75**	**6**	<1	<1	<1	<1	ND
2019	FOGO	C	FOGO-2019-C-2	60	<10	<100	ND	ND	<10	<10	<10	NT	**>1100**	**9.2**	**2**	<1	<1	<1	<1	ND
2019	FOGO	D	FOGO-2019-D-1	30	**90**	<100	ND	ND	<10	<10	<10	NT	**460**	**20**	**1**	<1	<1	<1	<1	ND
2019	FOGO	D	FOGO-2019-D-2	60	<10	<100	ND	ND	<10	<10	<10	NT	**93**	**21**	**3**	<1	<1	<1	<1	ND
2019	FOGO	E	FOGO-2019-E-1	30	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	**13**	**3**	**42**	**205**	<1	ND
2019	FOGO	E	FOGO-2019-E-2	n/a	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT
2019	FOGO	E	FOGO-2019-E-3	n/a	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT
2019	FOGO	E	FOGO-2019-E-4	60	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	**3**	<1	<1	**74**	<1	ND
2019	FOGO	F	FOGO-2019-F-1	30	<10	<100	ND	ND	<10	<10	<10	NT	**>1100**	**11**	**7**	<1	<1	<1	<1	ND
2019	FOGO	F	FOGO-2019-F-2	30	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	**3**	<1	<1	<1	<1	ND
2019	FOGO	F	FOGO-2019-F-3	60	<10	<100	ND	ND	<10	<10	<10	NT	<3	<3	**2**	<1	<1	<1	<1	ND
2019	FOGO	F	FOGO-2019-F-4	60	<10	<100	ND	ND	<10	<10	<10	NT	<3	<3	<1	<1	<1	<1	<1	ND
2019	FOGO	G	FOGO-2019-G-1	30	<10	<100	ND	ND	<10	<10	<10	NT	<3	<3	**6**	<1	<1	<1	<1	ND
2019	FOGO	G	FOGO-2019-G-2	n/a	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT
2019	FOGO	G	FOGO-2019-G-3	60	<10	<100	ND	ND	<10	<10	<10	NT	<3	<3	**1**	<1	<1	<1	<1	ND
2019	FOGO	H	FOGO-2019-H-1	30	<10	<100	ND	ND	<10	<10	<10	NT	**9.2**	<3	**2**	<1	<1	<1	<1	ND
2019	FOGO	H	FOGO-2019-H-2	30	<10	<100	ND	ND	<10	<10	<10	NT	**>1100**	**35**	**5**	<1	<1	<1	<1	ND
2019	FOGO	H	FOGO-2019-H-3	60	<10	<100	ND	ND	<10	<10	<10	NT	**93**	<3	**4**	<1	<1	**20**	<1	ND
2019	FOGO	H	FOGO-2019-H-4	60	<10	<100	ND	ND	<10	<10	<10	NT	**>1100**	**11**	**3**	<1	<1	<1	<1	ND
2019	FOGO	I	FOGO-2019-I-1	30	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	**6**	**1**	<1	**47**	<1	ND
2019	FOGO	I	FOGO-2019-I-2	60	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	<1	<1	<1	<1	<1	ND
2019	FOGO	J	FOGO-2019-J-1	30	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	**4**	<1	<1	<1	<1	ND
2019	FOGO	J	FOGO-2019-J-2	30	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	**7**	**2**	<1	<1	<1	ND
2019	FOGO	J	FOGO-2019-J-3	60	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	<1	<1	<1	<1	<1	ND
2019	FOGO	J	FOGO-2019-J-4	60	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	**5**	<1	<1	<1	<1	ND

Notes: CFU = colony forming unit; MPN = most probable number; <LOR = values reported as less than the limit of reporting; ND = values reported as not detected; NT = not tested

Table A2 Microbiological results for FOGO 2020–21 sampling

Sampling round	Organic waste group	De-identified facility / unit code	De-identified sample code	Sample depth	Group 17 – Bacteria and bacterial indicators										Group 18 – Helminths		Group 19 – Viruses			
					Clostridium perfringens	*Bacillus cereus*	*Salmonella* spp.	*Campylobacter* spp.	*Legionella* not *L.pneumophila*	*Legionella pneumophila* SG1	*Legionella pneumophila* SG2-15	Total *Legionella* Count	Thermotolerant Coliforms	*Escherichia coli*	*Taenia* sp. ova (intact eggs)	*Ascaris* sp. ova (intact eggs)	Enteroviruses	Adenoviruses	Reoviruses	Noroviruses
					CFU/g	CFU/g	/25g	CFU/g	CFU/mL	CFU/mL	CFU/mL	CFU/mL	MPN/g	MPN/g	/20 g (2019) /40g (2020/21)	/20 g (2019) /40g (2020/21)	/20 g (2019) /40g (2020/21)	/20 g (2019) /40g (2020/21)	/20 g (2019) /40g (2020/21)	/10g
2020/21	FOGO	A	FOGO-2020/21-A-1	30	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**9**	**3**	**57**	**86**	<1	NT
2020/21	FOGO	A	FOGO-2020/21-A-2	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**3**	<1	<1	<1	<1	NT
2020/21	FOGO	A	FOGO-2020/21-A-3	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**3**	<1	<1	<1	<1	NT
2020/21	FOGO	B	FOGO-2020/21-B-1	30	<10	**8800**	ND	<100	<10	<10	<10	<10	<3	<3	**4**	<1	<1	<1	<1	NT
2020/21	FOGO	B	FOGO-2020/21-B-2	60	<10	**4200**	ND	<100	<10	<10	<10	<10	<3	<3	<1	<1	<1	<1	<1	NT
2020/21	FOGO	B	FOGO-2020/21-B-3	60	<10	**4100**	ND	<100	<10	<10	<10	<10	<3	<3	<1	<1	<1	<1	<1	NT
2020/21	FOGO	C	FOGO-2020/21-C-1	30	<10	**200**	ND	<100	<10	<10	<10	<10	<3	<3	**3**	<1	<1	**36**	<1	NT
2020/21	FOGO	C	FOGO-2020/21-C-2	30	<10	**600**	ND	<100	<10	<10	<10	<10	**28**	**28**	**2**	<1	<1	**46**	<1	NT
2020/21	FOGO	C	FOGO-2020/21-C-3	30	<10	**200**	ND	<100	<10	<10	<10	<10	<3	<3	<1	<1	<1	<1	<1	NT
2020/21	FOGO	E	FOGO-2020/21-E-1	30	**110**	**500**	ND	<100	<10	<10	<10	<10	<3	<3	**4**	<1	<1	**91**	<1	NT
2020/21	FOGO	E	FOGO-2020/21-E-2	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	<1	<1	<1	<1	<1	NT
2020/21	FOGO	E	FOGO-2020/21-E-3	60	**80**	**300**	ND	<100	<10	<10	<10	<10	<3	<3	<1	<1	<1	<1	<1	NT
2020/21	FOGO	F	FOGO-2020/21-F-1	30	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**2**	<1	<1	**53**	<1	NT
2020/21	FOGO	F	FOGO-2020/21-F-2	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**1**	<1	<1	**48**	<1	NT
2020/21	FOGO	F	FOGO-2020/21-F-3	60	<10	<100	ND	<100	<10	<10	<10	<10	**3.6**	<3	**1**	<1	<1	**37**	<1	NT
2020/21	FOGO	G	FOGO-2020/21-G-1	30	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**11**	**2**	<1	**25**	<1	NT
2020/21	FOGO	G	FOGO-2020/21-G-2	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**4**	<1	<1	<1	<1	NT
2020/21	FOGO	G	FOGO-2020/21-G-3	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**3**	<1	<1	<1	<1	NT
2020/21	FOGO	H	FOGO-2020/21-H-1	30	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**6**	<1	<1	<1	<1	NT
2020/21	FOGO	H	FOGO-2020/21-H-2	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**1**	<1	<1	<1	<1	NT
2020/21	FOGO	H	FOGO-2020/21-H-3	60	**30**	<100	ND	<100	<10	<10	<10	<10	<3	<3	<1	<1	<1	<1	<1	NT
2020/21	FOGO	I	FOGO-2020/21-I-1	30	<10	**400**	ND	<100	<10	<10	<10	<10	<3	<3	**7**	<1	<1	**33**	<1	NT
2020/21	FOGO	I	FOGO-2020/21-I-2	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**6**	<1	<1	**14**	<1	NT
2020/21	FOGO	I	FOGO-2020/21-I-3	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**5**	<1	<1	<1	<1	NT
2020/21	FOGO	J	FOGO-2020/21-J-1	30	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	<1	<1	<1	<1	<1	NT
2020/21	FOGO	J	FOGO-2020/21-J-2	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	<1	<1	<1	<1	<1	NT
2020/21	FOGO	J	FOGO-2020/21-J-3	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	<1	<1	<1	<1	<1	NT
2020/21	FOGO	K	FOGO-2020/21-K-1	30	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**4**	<1	<1	<1	<1	NT
2020/21	FOGO	K	FOGO-2020/21-K-2	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**1**	<1	<1	<1	<1	NT
2020/21	FOGO	K	FOGO-2020/21-K-3	60	<10	**3200**	ND	<100	<10	<10	<10	<10	<3	<3	**1**	<1	<1	<1	<1	NT
2020/21	FOGO	L	FOGO-2020/21-L-1	30	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**8**	**3**	**41**	**79**	<1	NT
2020/21	FOGO	L	FOGO-2020/21-L-2	60	<10	**500**	ND	<100	<10	<10	<10	<10	<3	<3	**3**	<1	<1	<1	<1	NT
2020/21	FOGO	L	FOGO-2020/21-L-3	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	<1	<1	<1	<1	<1	NT
2020/21	FOGO	M	FOGO-2020/21-M-1	30	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**4**	<1	<1	<1	<1	NT
2020/21	FOGO	M	FOGO-2020/21-M-2	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**4**	<1	<1	<1	<1	NT
2020/21	FOGO	M	FOGO-2020/21-M-3	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**3**	<1	<1	<1	<1	NT
2020/21	FOGO	N	FOGO-2020/21-N-1	30	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**3**	**1**	<1	<1	<1	NT
2020/21	FOGO	N	FOGO-2020/21-N-2	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**2**	<1	<1	<1	<1	NT
2020/21	FOGO	N	FOGO-2020/21-N-3	60	<10	**200**	ND	<100	<10	<10	<10	<10	<3	<3	<1	<1	<1	<1	<1	NT

Notes: CFU = colony forming unit; MPN = most probable number; <LOR = values reported as less than the limit of reporting; ND = values reported as not detected; NT = not tested

Table A3 Microbiological results for GO 2020–21 sampling

Sampling round	Organic waste group	De-identified facility / unit code	De-identified sample code	Sample depth	Group 17 - Bacteria and bacterial indicators										Group 18 - Helminths		Group 19 - Viruses			
					Clostridium perfringens	*Bacillus cereus*	*Salmonella* spp.	*Campylobacter* spp.	*Legionella* not *L.pneumophila*	*Legionella pneumophila* SG1	*Legionella pneumophila* SG2-15	Total *Legionella* Count	Thermotolerant Coliforms	*Escherichia coli*	*Taenia* sp. ova (intact eggs)	*Ascaris* sp. ova (intact eggs)	Enteroviruses	Adenoviruses	Reoviruses	Noroviruses
					CFU/g	CFU/g	/25g	CFU/g	CFU/mL	CFU/mL	CFU/mL	CFU/mL	MPN/g	MPN/g	/20 g (2019) /40g (2020/21)	/20 g (2019) /40g (2020/21)	/20 g (2019) /40g (2020/21)	/20 g (2019) /40g (2020/21)	/20 g (2019) /40g (2020/21)	/10g
2020/21	GO	O	GO-2020/21-O-1	30	**1300**	**6000**	ND	<100	<10	<10	<10	<10	<3	<3	**5**	<1	<1	**53**	<1	NT
2020/21	GO	O	GO-2020/21-O-2	60	<10	**10000**	ND	<100	<10	<10	<10	<10	**35**	**35**	**1**	<1	<1	**14**	<1	NT
2020/21	GO	O	GO-2020/21-O-3	60	**1400**	**4000**	ND	<100	<10	<10	<10	<10	<3	<3	<1	<1	<1	<1	<1	NT
2020/21	GO	P	GO-2020/21-P-1	30	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**6**	<1	<1	<1	<1	NT
2020/21	GO	P	GO-2020/21-P-2	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**2**	<1	<1	<1	<1	NT
2020/21	GO	P	GO-2020/21-P-3	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**2**	<1	<1	<1	<1	NT
2020/21	GO	Q	GO-2020/21-Q-1	30	<10	**300**	ND	<100	<10	<10	<10	<10	**3.6**	**3.6**	**6**	<1	**25**	**38**	<1	NT
2020/21	GO	Q	GO-2020/21-Q-2	60	<10	**6700**	ND	<100	<10	<10	<10	<10	<3	<3	**2**	<1	<1	<1	<1	NT
2020/21	GO	Q	GO-2020/21-Q-3	60	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	<1	<1	<1	<1	<1	NT
2020/21	GO	R	GO-2020/21-R-1	30	**120**	<100	ND	<100	<10	<10	<10	<10	**7.4**	**7.4**	**9**	**2**	**80**	**955**	<1	NT
2020/21	GO	R	GO-2020/21-R-2	60	**20**	<100	ND	<100	<10	<10	<10	<10	<3	<3	**6**	<1	<1	**22**	<1	NT
2020/21	GO	R	GO-2020/21-R-3	60	**350**	<100	ND	<100	<10	<10	<10	<10	**35**	**20**	**2**	<1	<1	<1	<1	NT
2020/21	GO	S	GO-2020/21-S-1	30	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**6**	<1	<1	**28**	<1	NT
2020/21	GO	S	GO-2020/21-S-2	30	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	**4**	<1	<1	**95**	<1	NT
2020/21	GO	S	GO-2020/21-S-3	30	<10	<100	ND	<100	<10	<10	<10	<10	<3	<3	NT	NT	NT	NT	NT	NT

Notes: CFU = colony forming unit; MPN = most probable number; <LOR = values reported as less than the limit of reporting; ND = values reported as not detected; NT = not tested